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Bioinformatics Center
- Pathway Engineering -

Prof
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(D Sc)
[Adjunct Prof]

Scope of Research

This laborabory develops research on computational knowledge discovery, e.g. inference of pathway information from gene expression profile data, and simulation system for cells and organisms through the biopathway simulation of gene regulatory networks, signaling pathways, metabolic pathways, and physical simulations, etc. With this approach, the functions of genes and systems of genes will be analyzed and predicted.

Research Activities (Year 2003)

Presentations

Gene Networks: Inference, Modeling and Simulation, Miyano S, Seminar on Functional Genomics, AAAS Annual Meeting and Science 2003, Denver, USA, 16 February 2003.

Estimating gene networks from gene expression data by combining Bayesian network model with promoter element detection, Tamada Y, Kim S, Bannai H, Imoto S, Tashiro K, Kuhara S, Miyano S, European Conference on Computational Biology 2003, Paris, France, 27-30, September 2003.

Inference, Modeling and Simulation of Gene Networks, Miyano S, First International Workshop on Computational Methods in Systems Biology, Rovereto, Italy, 24-26 February, 2003.

Towards biopathway modeling and simulation, Miyano, S, The 24th International Conference on Application and Theory of Petri Nets, Eindhoven, The Netherlands, 23-28 July, 2003.

Boundary formation by Notch signaling in Drosophila multicellular systems: experimental observations and gene network modeling by Genomic Object Net, Matsuno H, Murakami R, Yamane R, Yamasaki N, Fujita S, Yoshimori H, Miyano S, The Eighth Pacific Symposium on Biocomputing, Hawaii, USA, 3-7 January, 2003.

Combining microarrays and biological knowledge for estimating gene networks via Bayesian networks, Imoto S, Higuchi T, Goto T, Tashiro K., Kuhara S, Miyano S, The Second International Conference on Computational Systems Bioinformatics, Stanford University, USA, 12-14 August, 2003.

Grants

Miyano S, Research on Information Technology for Gene Network Analysis, Grant-in-Aid for Scientific Research on Priority Areas (C), "Genome Information Science" from MEXT, 1 April 2003-31 March 2004.

Miyano S, Foundations of Computational Knowledge Discovery from Proteome Data, Grant-in-Aid for Scientific Research (B)(1), 1 April 2003 - 31 March 2006.

* Professor Satoru Miyano finished his appointment as adjunct professor on March 31, 2003.

Computational Challenges in Systems Biology.

Systems biology can be explored by development of computational tools and capabilities which enable us to understand complex biological systems. Scientific contributions are strongly anticipated to produce practical benefits such as biomedical applications, solutions for environmental problems, etc. For this purpose, gene networks will play a central role in systems biology and computational challenges to inferring, modeling and simulating biological systems are receiving more attentions.

Advances in measurement technology have enabled genome-wide biological data production. Our challenge in this scope is comprised of two approaches.

The first is "how to create gene network information". For this direction, we have developed three kinds of computational methods for inferring gene networks from gene expression profile data obtained from various perturbations such as gene disruptions, shocks, etc. We developed a method which can analyze the continuous data and automatically detect linear and even nonlinear relationships between genes. We employed nonparametric regression for capturing nonlinear relationships between genes and derive a new criterion called BNRC (Bayesian Network and Nonlinear Regression) for choosing the network in general situations. We also extended this method to dynamic Bayesian network and nonparametric heteroscedastic regression that can cope with time-course microarray data. We have also developed a computational strategy to employ other biological data such as protein-protein interaction data to refine gene networks (Fig. 1). Furthermore, we have developed a gene network analysis tool for extracting subnetworks (Fig. 2).

The second is "how to model and simulate gene networks". Obviously, an important challenge is a creation of a platform with which biological scientists can comfortably model and simulate dynamic causal interactions and processes in the cell such as gene regulations, metabolic pathways, and signal transduction cascades. For this direction, we have developed a software tool Genomic Object Net (GON) (http://www.genomicobject.net/) for biopathway modeling and simulation. We also have developed GONML for describing dynamic biological systems, and simultaneously we have developed a system which converts biopathway models compiled in KEGG and BioCyc to the GONML. Especially, all metabolic pathway models in KEGG are now ready for re-modeling and simulation with GON. With this system, various metabolic pathway information were integrated into a big pathway map so that it can be simulated with GON (Fig. 3).

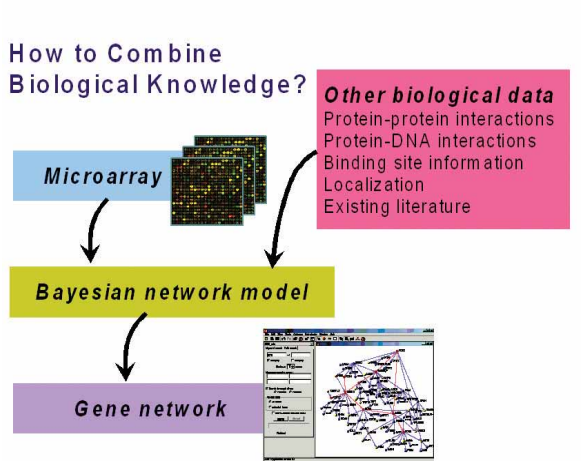

Fig. 1 Employing bilogical information to refine gene network estimation.

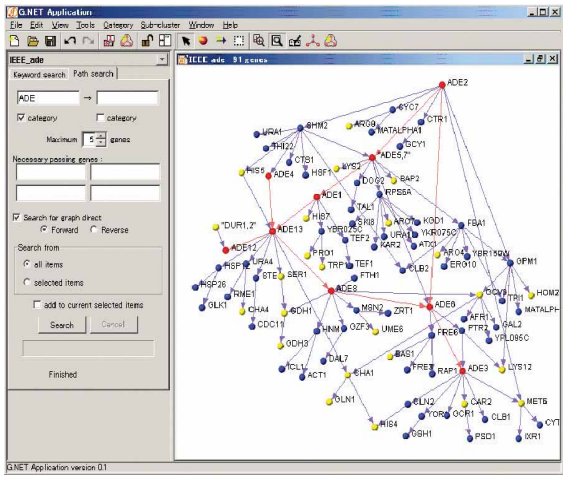

Fig. 2 Gene network analysis tool for network information extraction.

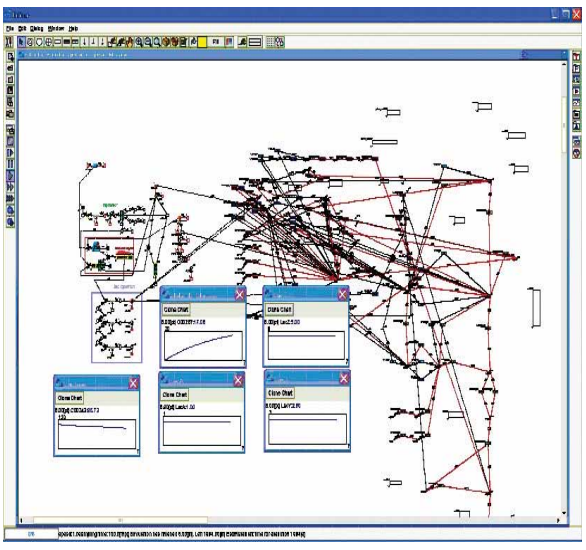

Fig. 3 Modeling and simulation of lac operon gene regulatory network together with metabolic pathways on Genomic Object Net.